

#48,80

RESULT 1

S18921

genome polyprotein - bean yellow mosaic virus (fragment)

N;Contains: 6K protein; coat protein; cylindrical inclusion protein; proteinase

N1a; RNA-directed RNA polymerase (EC 2.7.7.48) N1b

C;Species: bean yellow mosaic virus, BYMV

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Nov-2000

C;Accession: S18921; S22484; S11208

R;Boye, K.; Stummann, B.M.; Henningsen, K.W.

submitted to the EMBL Data Library, November 1991

A;Description: cDNA sequence of the Bean Yellow Mosaic Virus nuclear inclusion protein genes.

A;Reference number: S18921

A;Accession: S18921

A;Molecule type: genomic RNA

A;Residues: 1-1372 <BOY>

A;Cross-references: EMBL:X63358

R;Boye, K.; Stummann, B.M.; Henningsen, K.W.

Plant Mol. Biol. 18, 1203-1205, 1992

A;Title: cDNA cloning and sequencing of the bean yellow mosaic virus nuclear inclusion protein genes.

A;Reference number: S22484; MUID:92288317

A;Accession: S22484

A;Molecule type: genomic RNA

A;Residues: 146-849, 'R', 852-1099 <BO2>

A;Cross-references: EMBL:X63358

R;Boye, K.; Jensen, P.E.; Stummann, B.M.; Henningsen, K.W.

Nucleic Acids Res. 18, 4926, 1990

A;Title: Nucleotide sequence of cDNA encoding the BYMV coat protein gene.

A;Reference number: S11208; MUID:90370489

A;Accession: S11208

A;Molecule type: genomic RNA

A;Residues: 1100-1372 <BOW>

A;Cross-references: EMBL:X53684; NID:g61217; PIDN:CAA37724.1; PID:g61218

C;Superfamily: tobacco etch virus genome polyprotein

C;Keywords: coat protein; cylindrical inclusion protein; genome-linked protein; inclusion protein; nucleotidyltransferase; nucleus; phosphoprotein; polyprotein; proteinase

F;1-92/Product: cylindrical inclusion protein (fragment) #status predicted <CIP>

F;93-145/Product: 6K protein #status predicted <VPT>

F;146-579/Product: proteinase N1a #status predicted <N1A>

F;580-1099/Product: RNA-directed RNA polymerase N1b #status predicted <RRP>

F;1100-1372/Product: coat protein #status predicted <CPR>

F;208/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 71.3%; Score 1627; DB 2; Length 1372;

Best Local Similarity 68.0%; Pred. No. 5.1e-120;

Matches 295; Conservative 64; Mismatches 75; Indels 0; Gaps 0;

Qy 1 GKSKRTRQKLKFRARDMKDRYEVHADEGTLVENFGTRYSKKGKTKGTVVGLGAKTRRFT 60

||:||||:||||:| |||||:| ||:||| |: |||||:|:|||| ||| ||| |||

Db 146 GKNKRTKQKLRFDRDARMKNRVEVYADEETITENFGSKYTKKGKVKGTTVGMGKTKTRRFT 205

Qy 61 NMYGFDPTSEYFARYLDPITGATLDETPIHNVNLVAEHFGDIRLDMVDKELLDKQHLYLK 120

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 206 NMYGFDPTSEYFARYLDPITGETLDEQPITNLNLISEHFQEMRRKYIENDVMEAQHFTSN 265

Qy	121	RPIECYFVKDAGQKVMRIDLTPHNPLLASDVSTTIMGYPEREGELRQTGKARLVDPSLEP	180
		::                         :	
Db	266	PRIEAYFVKDAGQKVLKVDLTPHKPLLYSDKHGNIMGYPEREGELRQTGTAEFVDPKDLP	325
Qy	181	ARNEDIDAEFESLNRISGLRDYNPISQNVCLLTNESEGHREKMFYGIGYSVIITNQHLFR	240
		::       :             ::   :	
Db	326	ESKETADFGFESLSKIGGLRDYNPIASNVCLLENESAHCDEIFGIGYGNVIITNQHLFR	385
Qy	241	RNNGELSIQSKHG YFRCRNTTSLKMLPLEGHDILLIQLPRDFPVPFPQKIRFREPRVDDKI	300
		: :      : :   : : : : : : : : : : : : : : :	
Db	386	HNNGELTIKSKHGTFCKKNTCALKLLPIDGHDLLLIQMPKDFPVPFPQKLRFREPTHEDKI	445
Qy	301	VLVSTNFQEKSSSSTVSESSNISRVQSANFYKHWISTVAGHCGNPMVSTKDGFI VGIHSL	360
		:    :      :	
Db	446	VLVSTNFQEKSFSSSVSESSNISRVKQANFFKHWISTIAGQCGNPMVSTKDGFI VGIHSL	505
Qy	361	ASLTGVDNIFTSFPPQFENKYLQKLSEHTWCSGWKLNLGKISWGGINIVEDAPEEPFITS	420
		:::   : :          :  : : :          :          :   : :	
Db	506	TAVSGDLNVFTSIPQNFEEIILKQINKKNWCCGWKLNTAQIGWDGIKIVDDQPKDPFPVS	565
Qy	421	KMASLLSDLNCSFQ	434
		:	
Db	566	KMAGLLNDLQLSFQ	579